

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In the Application of:

S. C. FALCO ET AL.

CASE NO.: BB1336 US CNT

APPLICATION NO.: UNKNOWN

GROUP ART UNIT: UNKNOWN

FILED: HEREWITH

EXAMINER: UNKNOWN

FOR: PLANT PROTEINASES

**PRELIMINARY AMENDMENT**

Commissioner of Patents and Trademarks  
Washington, D.C. 20231

Sir:

Prior to examination, please amend the captioned application as follows and consider the following remarks.

**IN THE SPECIFICATION:**

**Please replace the following paragraphs:**

**Paragraph beginning at page 1, line 3:**

This application is a continuation of U.S. Application No. 09/501,423, filed February 9, 2000, which claims the benefit of U.S. Provisional Application No. 60/119,599, filed February 10, 1999, whose contents are hereby incorporated by reference.

**Paragraph beginning at page 2, line 13:**

The present invention relates to isolated polynucleotides comprising a nucleotide sequence encoding a polypeptide of at least 40 amino acids that has at least 85% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of a calpain p94 polypeptide of SEQ ID NOs:2, 4, 6, 8, 10, and 12. The present invention also relates to an isolated polynucleotide comprising the complement of the nucleotide sequences described above.

**Paragraph beginning at page 2, line 19:**

The present invention relates to isolated polynucleotides comprising a nucleotide sequence encoding a polypeptide of at least 150 amino acids that has at least 95% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of a cysteine protease 1 polypeptide of SEQ ID NOs:14, 16, 18, and 20. The present invention also relates to an isolated polynucleotide comprising the complement of the nucleotide sequences described above.

**Paragraph beginning at page 2, line 25:**

The present invention relates to isolated polynucleotides comprising a nucleotide sequence encoding a polypeptide of at least 200 amino acids that has at least 80% identity

based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of a cysteine protease 2 polypeptide of SEQ ID NOs:22 and 24. The present invention also relates to an isolated polynucleotide comprising the complement of the nucleotide sequences described above.

**Paragraph beginning at page 2, line 31:**

The present invention relates to isolated polynucleotides comprising a nucleotide sequence encoding a polypeptide of at least 175 amino acids that has at least 95% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of a CLPA polypeptide of SEQ ID NOs:26, 34, 30, 32, 28, and 36. The present invention also relates to an isolated polynucleotide comprising the complement of the nucleotide sequences described above.

**Paragraph beginning at page 2, line 37:**

The present invention relates to isolated polynucleotides comprising a nucleotide sequence encoding a CLPP polypeptide selected from the group consisting of SEQ ID NOs:38, 40, 42, 44, 46, 48, 50, 52, 54, and 56. The present invention also relates to an isolated polynucleotide comprising the complement of the nucleotide sequences described above.

**Paragraph beginning at page 3, line 25:**

The present invention relates to a calpain p94 polypeptide of at least 40 amino acids comprising at least 85% homology based on the Clustal method of alignment compared to a polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 6, 8, 10, and 12.

**Paragraph beginning at page 3, line 28:**

The present invention relates to a cysteine protease 1 polypeptide of at least 150 amino acids comprising at least 95% homology based on the Clustal method of alignment compared to a polypeptide selected from the group consisting of SEQ ID NOs:14, 16, 18, and 20.

**Paragraph beginning at page 3, line 32:**

The present invention relates to a cysteine protease 2 polypeptide of at least 200 amino acids comprising at least 80% homology based on the Clustal method of alignment compared to a polypeptide selected from the group consisting of SEQ ID NOs:22 and 24.

**Paragraph beginning at page 3, line 35:**

The present invention relates to a CLPA polypeptide of at least 175 amino acids comprising at least 95% homology based on the Clustal method of alignment compared to a polypeptide selected from the group consisting of SEQ ID NOs:26, 34, 30, 32, 28, and 36.

**Paragraph beginning at page 4, line 1:**

The present invention relates to a CLPP polypeptide selected from the group consisting of SEQ ID NOs:38, 40, 42, 44, 46, 48, 50, 52, 54, and 56.

**Table 1, bridging pages 5 and 6:**

**TABLE 1**  
**PLANT PROTEINASES**

Protein	Clone Designation	SEQ ID NO:	
		(Nucleotide)	(Amino Acid)
Corn Calpain p94 Subunit	cbn2.pk0039.c2	1	2
Rice Calpain p94 Subunit	rsl1n.pk013.h14	3	4
Soybean Calpain p94 Subunit	ses9c.pk001.j23	5	6
Rice Cysteine Protease 1	rr1.pk084.j16	13	14
Wheat Cysteine Protease 1	Contig of: wdk1c.pk009.j19 wre1n.pk164.b11	15	16
Soybean Cysteine Protease 2	Contig of: sgs2c.pk002.p14 srr3c.pk003.d10 scb1c.pk003.d8	21	22
Corn CLP ATP Binding Subunit	p0110.cgsmk69r	25	26
Rice CLP ATP Binding Subunit	Contig of: rlr6.pk0083.f9 rlr24.pk0088.f7 rlr6.pk0029.d7	33	34
Wheat CLP ATP Binding Subunit	wlm96.pk032.n8	29	30
Corn CLP Proteolytic Subunit	p0060.coran66r	37	38
Rice CLP Proteolytic Subunit	rsr9n.pk004.p5	39	40
Soybean CLP Proteolytic Subunit	scb1c.pk004.k24	41	42
Wheat CLP Proteolytic Subunit	wle1n.pk0042.f7	43	44
Wheat CLP Proteolytic Subunit	wlk8.pk0006.a4	45	46
Corn Calpain p94 Subunit	cbn2.pk0039.c2: fis	7	8
Rice Calpain p94 Subunit	rsl1n.pk013.h14: fis	9	10
Soybean Calpain p94 Subunit	ses9c.pk001.j23: fis	11	12
Rice Cysteine Protease 1	rr1.pk084.j16: fis	17	18
Wheat Cysteine Protease 1	wdk1c.pk009.j19: fis	19	20
Soybean Cysteine Protease 2	srr3c.pk003.d10: fis	23	24
Corn CLP ATP Binding Subunit	p0110.cgsmk69r: fis	31	32
Rice CLP ATP Binding Subunit	rlr24.pk0088.f7: fis	27	28
Wheat CLP ATP Binding Subunit	wlm96.pk032.n8: fis	35	36
Corn CLP Proteolytic Subunit	p0060.coran66r: fis	47	48
Rice CLP Proteolytic Subunit	rsr9n.pk004.p5: fis	49	50

Soybean CLP Proteolytic Subunit	scb1c.pk004.k24:fis	51	52
Wheat CLP Proteolytic Subunit	wle1n.pk0042.f7:fis	53	54
Wheat CLP Proteolytic Subunit	wlk8.pk0006.a4:fis	55	56

**Paragraph beginning at page 22, line 16:**

The data in Table 5 represents a calculation of the percent identity of the amino acid sequences set forth in SEQ ID NOs:2, 4, 6, 8, 10, and 12 and the *Drosophila melanogaster* sequences (NCBI General Identifier Nos. 600420 and 1079058).

**Table 5 beginning at page 22, line 20:**

TABLE 5

Percent Identity of Amino Acid Sequences Deduced From the Nucleotide Sequences of cDNA Clones Encoding Polypeptides Homologous to Calpain p94

SEQ ID NO.	Percent Identity to	
	600420	1079058
2	50.0	50.0
4	57.4	57.4
6	52.0	52.0
8	25.8	25.8
10	24.9	24.9
12	26.0	26.0

**Paragraph beginning at page 24, line 1:**

Amino acid sequence alignments using the Clustal method of alignment indicates that the rice sequence starts 88 amino acids down stream from the corn starting methionine, and that the wheat sequence starts 163 amino acids down stream from the corn starting methionine. The corn sequence has a signal sequence (amino acids 1-19) and a mature protein which corresponds to amino acids 137 through 371. Thus, the rice and wheat sequences included here contain the entire mature protein. The data in Table 8 represents a calculation of the percent identity of the amino acid sequences set forth in SEQ ID NOs:14, 16, 18, and 20 and the *Zea mays* sequence (NCBI General Identifier No. 1706260).

**Table 8 beginning at page 24, line 10:**

TABLE 8

Percent Identity of Amino Acid Sequences Deduced From the Nucleotide Sequences of cDNA Clones Encoding Polypeptides Homologous to Cysteine Protease 1

SEQ ID NO.	Percent Identity to	
	1706260	
14	88.0	
16	87.1	

18	90.9
20	86.3

**Paragraph beginning at page 25, line 16:**

The data in Table 11 represents a calculation of the percent identity of the amino acid sequences set forth in SEQ ID NOs:22 and 24 and the *Phaseolus vulgaris* sequence (NCBI General Identifier No. 2511691).

**Table 11 beginning at page 25, line 20:**

TABLE 11

Percent Identity of Amino Acid Sequences Deduced From the Nucleotide  
Sequences of cDNA Clones Encoding Polypeptides  
Homologous to Cysteine Protease 2

SEQ ID NO.	Percent Identity to	
	2511691	
22	67.9	
24	75.1	

**Paragraph beginning at page 27, line 5:**

The data in Table 14 represents a calculation of the percent identity of the amino acid sequences set forth in SEQ ID NOs:26, 34, 30, 32, 28, and 36 and the *Lycopersicon esculentum* sequences (NCBI General Identifier Nos. 399213 and 399212).

**Table 14 beginning at page 27, line 9:**

TABLE 14

Percent Identity of Amino Acid Sequences Deduced From the Nucleotide  
Sequences of cDNA Clones Encoding Polypeptides  
Homologous to CLP Protease ATP-Binding Subunit

SEQ ID NO.	Percent Identity to	
	399213	399212
26	92.2	92.2
34	80.9	79.9
30	86.5	87.1
32	86.9	86.0
28	90.8	89.6
36	88.7	87.4

**Paragraph beginning at page 28, line 26:**

The data in Table 17 represents a calculation of the percent identity of the amino acid sequences set forth in SEQ ID NOs:38, 40, 42, 44, 46, 48, 50, 52, 54, and 56 and the *Arabidopsis thaliana* and *Azospirillum brasilense* sequences (NCBI General Identifier Nos. 5360593, 4887543, and 6685315).

**Table 17 beginning at page 29, line 4:**

**TABLE 17**

Percent Identity of Amino Acid Sequences Deduced From the Nucleotide  
Sequences of cDNA Clones Encoding Polypeptides  
Homologous to CLP Protease Proteolytic Subunit

SEQ ID NO.	Percent Identity to		
	5360593	4887543	6685315
38	78.8	52.2	53.1
40	44.0	55.0	73.4
42	48.7	97.3	58.7
44	55.8	91.6	63.2
46	57.1	64.3	81.0
48	78.8	39.7	38.6
50	34.0	43.8	57.6
52	45.5	92.5	51.5
54	39.0	47.1	60.5
56	48.9	87.9	54.6

**IN THE CLAIMS:**

**Please replace the following claims:**

1. "amended" An isolated polynucleotide comprising a first nucleotide sequence encoding a polypeptide of at least 40 amino acids that has at least 85% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 6, 8, 10, and 12,

or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

2. "amended" An isolated polynucleotide comprising a first nucleotide sequence encoding a polypeptide of at least 150 amino acids that has at least 95% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:14, 16, 18, and 20,

or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

3. "amended" An isolated polynucleotide comprising a first nucleotide sequence encoding a polypeptide of at least 200 amino acids that has at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:22 and 24,

or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

4. "amended" An isolated polynucleotide comprising a first nucleotide sequence encoding a polypeptide of at least 175 amino acids that has at least 95% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:26, 34, 30, 32, 28, and 36,

or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

5. "amended" An isolated polynucleotide comprising a first nucleotide sequence encoding a polypeptide selected from the group consisting of SEQ ID NOs:38, 40, 42, 44, 46, 48, 50, 52, 54, and 56,

or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

14. "amended" A polypeptide of at least 40 amino acids that has at least 85% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 6, 8, 10, and 12.

15. "amended" A polypeptide of at least 150 amino acids that has at least 95% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:14, 16, 18, 20.

16. "amended" A polypeptide of at least 200 amino acids that has at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:22 and 24.

17. "amended" A polypeptide of at least 175 amino acids that has at least 95% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:26, 34, 30, 32, 28, and 36.

18. "amended" A polypeptide selected from the group consisting of SEQ ID NOs:38, 40, 42, 44, 46, 48, 50, 52, 54, and 56.

**IN THE ABSTRACT:**

**Please replace the paragraph beginning at page 39, line 4, with the following:**

Isolated polynucleotides from corn (*Zea mays*), rice (*Oryza sativa*), soybean (*Glycine max*), and wheat (*Triticum aestivum*) encoding proteinases. Also provided is the construction of a chimeric gene encoding all or a portion of the proteinase, in sense or antisense orientation, wherein expression of the chimeric gene results in production of altered levels of the proteinase in a transformed host cell.

### REMARKS

In the parent application, U.S. Application No. 09/501,423, Applicants filed a Request for Continued Examination on November 29, 2001 in order to prosecute what Applicants' representative believed to be the elected invention, i.e., Group II drawn to isolated polynucleotides encoding cysteine protease 1 or cysteine protease 2 polypeptides (which corresponds to SEQ ID NOs:13-24 of the corrected application).

An Office Communication mailed January 29, 2002, however, indicated that Applicants' elected invention of the parent application is directed to SEQ ID NOs:7-12 and 35-40, which correspond to polypeptides having a function different from cysteine protease 1 or cysteine protease 2. In particular, SEQ ID NOs:7-12 are directed to calpain 94 subunits, SEQ ID NOs:35 and 36 are directed to CLP ATP binding subunits, and SEQ ID NOs:37-40 are directed to CLP proteolytic subunits.

Applicants' representative appreciates the courtesies extended by Examiners Kerr and Stanton during a telephone interview on February 6, 2002. During that interview, the filing of a continuation application was discussed.

In the present Preliminary Amendment, Applicants provide amendments to the specification and claims that correct an administrative error of the parent application. The amendments to the application are for the purpose of curing defects and it is submitted that these amendments are obvious to one skilled in the art. Accordingly, no new matter is believed to be entered by these amendments.

To demonstrate that the following amendments are supported in the originally filed application, Applicants submit the enclosed Appendix and the following detailed discussion. The Appendix provides the percent identities (obtained using the Clustal alignment method) between the amino acid sequences of SEQ ID NOs:2-56 and the sequences having NCBI general identifier numbers 600420, 1079058, 1706260, 2511691, 399213, 399212, 5360593, 4887543, 6685315 which are discussed throughout the specification. In considering the following detailed discussion, it may be helpful for the Examiner to refer to the marked up copy of Table 1 submitted herewith, which lists the plant proteinases of the application.

#### Rice Cysteine Protease 1 having clone designation rr1.pk084.j16

In the amended tables, SEQ ID NOs:7 and 8 were replaced, respectively, with SEQ ID NOs:13 and 14, as a rice cysteine protease 1. This amendment is supported by the following:

- (i) the as-filed Sequence Listing indicates that SEQ ID NOs:13 and 14 are from rice;
- (ii) originally filed Table 6 includes clone designation rr1.pk084.j16 in the BLAST results for sequences encoding polypeptides homologous to cysteine protease 1; and
- (iii) the enclosed Appendix demonstrates that SEQ ID NO:14, rather than SEQ ID NO:8, has 88.0% identity to NCBI General Identifier No. 1706260. (See, originally filed Table



8 and Example 4.) None of the other sequences in the application has 88.0% identity to NCBI General Identifier No. 1706260.

Wheat Cysteine Protease 1 having clone designation contig of wdk1c.pk009.j19 and wre1n.pk164.b11

In the amended tables, SEQ ID NOs:9 and 10 were replaced, respectively, with SEQ ID NOs:15 and 16, as a wheat cysteine protease 1. This amendment is supported by the following:

- (i) the as-filed Sequence Listing indicates that SEQ ID NOs:15 and 16 are from wheat;
- (ii) originally filed Table 6 includes clone designation contig of wdk1c.pk009.j19 and wre1n.pk164.b11 in the BLAST results for sequences encoding polypeptides homologous to cysteine protease 1; and
- (iii) the enclosed Appendix demonstrates that SEQ ID NO:16, rather than SEQ ID NO:9, has 87.1% identity to NCBI General Identifier No. 1706260. (See, originally filed Table 8 and Example 4). None of the other sequences in the application has 87.1% identity to NCBI General Identifier No. 1706260.

Soybean Cysteine Protease 2 having clone designation contig of sgs2c.pk002.p14, srr3c.pk003.d10, and scb1c.pk003.d8

In the amended tables, SEQ ID NOs:11 and 12 were replaced, respectively, with SEQ ID NOs:21 and 22, as a soybean cysteine protease 2. This amendment is supported by the following:

- (i) the as-filed Sequence Listing indicates that SEQ ID NOs:21 and 22 are from soybean;
- (ii) originally filed Table 9 includes clone designation contig of sgs2c.pk002.p14, srr3c.pk003.d10, and scb1c.pk003.d8 in the BLAST results for sequences encoding polypeptides homologous to cysteine protease 2; and
- (iii) the enclosed Appendix demonstrates that SEQ ID NO:22, rather than SEQ ID NO:12, has 67.9% identity to NCBI General Identifier No. 2511691. (See, originally filed Table 11 and Example 5). None of the other sequences in the application has 67.9% identity to NCBI General Identifier No. 2511691.

Corn CLP ATP Binding Subunit having clone designation p0110.cgsmk69r

In the amended tables, SEQ ID NOs:13 and 14 were replaced, respectively, with SEQ ID NOs:25 and 26. This amendment is supported by the following:

- (i) the as-filed Sequence Listing indicates that SEQ ID NOs:25 and 26 are from corn;

(ii) originally filed Table 12 includes clone designation p0110.cgsmk69r in the BLAST results for sequences encoding polypeptides homologous to CLP protease ATP binding subunit; and

(iii) the enclosed Appendix demonstrates that SEQ ID NO:26, rather than SEQ ID NO:14, has 92.2% identity to NCBI General Identifier Nos. 399213 and 399212. (See, originally filed Table 14 and Example 6). None of the other sequences in the application has 92.2% identity to NCBI General Identifier Nos. 399213 and 399212.

Rice CLP ATP Binding Subunit having clone designation contig of rlr6.pk0083.f9, rlr24.pk0088.f7, and rlr6.pk0029.d7

In the amended tables, SEQ ID NOs:15 and 16 were replaced, respectively, with SEQ ID NOs:33 and 34. This amendment is supported by the following:

(i) the as-filed Sequence Listing indicates that SEQ ID NOs:33 and SEQ ID NO:34 are from rice; and

(ii) the enclosed Appendix demonstrates that SEQ ID NO:34, rather than SEQ ID NO:16, has 80.9% and 79.9% identity, respectively, to NCBI General Identifier Nos. 399213 and 399212. (See, originally filed Table 14 and Example 6). None of the other sequences in the application has 80.9% and 79.9% identity, respectively, to NCBI General Identifier Nos. 399213 and 399212.

Wheat CLP ATP Binding Subunit having clone designation wlm96.pk032.n8

In the amended tables, SEQ ID NOs:17 and 18 were replaced, respectively, with SEQ ID NOs:29 and 30. This amendment is supported by the following:

(i) the as-filed Sequence Listing indicates that SEQ ID NOs:29 and SEQ ID NO:30 are from wheat;

(ii) originally filed Table 12 includes clone designation wlm96.pk032.n8 in the BLAST results for sequences encoding polypeptides homologous to CLP protease ATP binding subunit; and

(iii) the enclosed Appendix demonstrates that SEQ ID NO:30, rather than SEQ ID NO:18, has 86.5% and 87.1% identity, respectively, to NCBI General Identifier Nos. 399213 and 399212. (See, originally filed Table 14 and Example 6). None of the other sequences in the application has 86.5% and 87.1% identity, respectively, to NCBI General Identifier Nos. 399213 and 399212.

Corn CLP Proteolytic Subunit having clone designation p0060.coran66r

In the amended tables, SEQ ID NOs:19 and 20 were replaced, respectively, with SEQ ID NOs:37 and 38. This amendment is supported by the following:

(i) the as-filed Sequence Listing indicates that SEQ ID NOs:37 and SEQ ID NO:38 are from corn;

(ii) originally filed Table 15 includes clone designation p0060.coran66r in the BLAST results for sequences encoding polypeptides homologous to CLP protease proteolytic subunit; and

(iii) the enclosed Appendix demonstrates that SEQ ID NO:38, rather than SEQ ID NO:20, has 78.8%, 52.2%, and 53.1% identity, respectively, to NCBI General Identifier Nos. 5360593, 4887543, and 6685315. (See, originally filed Table 17 and Example 7). None of the other sequences in the application has 78.8%, 52.5%, and 53.1% identity, respectively, to NCBI General Identifier Nos. 5360593, 4887543, and 6685315.

Rice CLP Proteolytic Subunit having clone designation rsr9n.pk004.p5

In the amended tables, SEQ ID NOs:21 and 22 were replaced, respectively, with SEQ ID NOs:39 and 40. This amendment is supported by the following:

(i) the as-filed Sequence Listing indicates that SEQ ID NOs:39 and 40 are from rice;

(ii) originally filed Table 15 includes clone designation rsr9n.pk004.p5 in the BLAST results for sequences encoding polypeptides homologous to CLP protease proteolytic subunit; and

(iii) the enclosed Appendix demonstrates that SEQ ID NO:40, rather than SEQ ID NO:22, has 44.0%, 55.0%, and 73.4% identity, respectively, to NCBI General Identifier Nos. 5360593, 4887543, and 6685315. (See, originally filed Table 17 and Example 7.) None of the other sequences in the application has 44.0%, 55.0%, and 73.4% identity, respectively, to NCBI General Identifier Nos. 5360593, 4887543, and 6685315.

Soybean CLP Proteolytic Subunit having clone designation scb1c.pk004.k24

In the amended tables, SEQ ID NOs:23 and 24 were replaced, respectively, with SEQ ID NOs:41 and 42. This amendment is supported by the following:

(i) the as-filed Sequence Listing indicates that SEQ ID NOs:41 and 42 are from soybean;

(ii) originally filed Table 15 includes clone designation scb1c.pk004.k24 in the BLAST results for sequences encoding polypeptides homologous to CLP protease proteolytic subunit; and

(iii) the enclosed Appendix demonstrates that SEQ ID NO:42, rather than SEQ ID NO:24, has 48.7%, 97.3%, and 58.7% identity, respectively, to NCBI General Identifier Nos. 5360593, 4887543, and 6685315. (See, originally filed Table 17 and Example 7.) None of the other sequences in the application has 48.7%, 97.3%, and 58.7% identity, respectively, to NCBI General Identifier Nos. 5360593, 4887543, and 6685315.

Wheat CLP Proteolytic Subunit having clone designation wle1n.pk0042.f7

In the amended tables, SEQ ID NOs:25 and 26 were replaced, respectively, with SEQ ID NOs:43 and 44. This amendment is supported by the following:

(i) the as-filed Sequence Listing indicates that SEQ ID NOs:43 and 44 are from wheat;  
(ii) originally filed Table 15 includes clone designation wle1n.pk0042.f7 in the BLAST results for sequences encoding polypeptides homologous to CLP protease proteolytic subunit;  
and

(iii) the enclosed Appendix demonstrates that SEQ ID NO:44, rather than SEQ ID NO:26, has 55.8%, 91.6%, and 63.2% identity, respectively, to NCBI General Identifier Nos. 5360593, 4887543, and 6685315. (See, originally filed Table 17 and Example 7.) None of the other sequences in the application has 55.8%, 91.6%, and 63.2% identity, respectively, to NCBI General Identifier Nos. 5360593, 4887543, and 6685315.

Wheat CLP Proteolytic Subunit having clone designation wlk8.pk0006.a4

In the amended tables, SEQ ID NOs:27 and 28 were replaced, respectively, with SEQ ID NOs:45 and 46. This amendment is supported by the following:

(i) the as-filed Sequence Listing indicates that SEQ ID NOs:45 and 46 are from wheat;  
(ii) originally filed Table 15 includes clone designation wlk8.pk0006.a4 in the BLAST results for sequences encoding polypeptides homologous to CLP protease proteolytic subunit;  
and

(iii) the enclosed Appendix demonstrates that SEQ ID NO:46, rather than SEQ ID NO:28, has 57.1%, 64.3%, and 81.0% identity, respectively, to NCBI General Identifier Nos. 5360593, 4887543, and 6685315. (See, originally filed Table 17 and Example 7.) None of the other sequences in the application has 57.1%, 64.3%, and 81.0% identity, respectively, to NCBI General Identifier Nos. 5360593, 4887543, and 6685315.

Corn Calpain p94 Subunit having clone designation cbn2.pk0039.c2:fis

In the amended tables, SEQ ID NOs:29 and 30 were replaced, respectively, with SEQ ID NOs:7 and 8. This amendment is supported by the following:

(i) the as-filed Sequence Listing indicates that SEQ ID NOs:7 and 8 are from corn;  
(ii) originally filed Table 4 includes clone designation cbn2.pk0039.c2:fis in the BLAST results for sequences encoding polypeptides homologous to calpain p94; and  
(iii) the enclosed Appendix demonstrates that SEQ ID NO:8, rather than SEQ ID NO:30, has 25.8% identity to NCBI General Identifier Nos. 600420 and 1079058. (See, originally filed Table 5 and Example 3.) None of the other sequences in the application has 25.8% identity to NCBI General Identifier Nos. 600420 and 1079058.

Rice Calpain p94 Subunit having clone designation rs11n.pk013.h14:fis

In the amended tables, SEQ ID NOs:31 and 32 were replaced, respectively, with SEQ ID NOs:9 and 10. This amendment is supported by the following:

- (i) the as-filed Sequence Listing indicates that SEQ ID NOs:9 and 10 are from rice;
- (ii) originally filed Table 4 includes clone designation rs11n.pk013.h14:fis in the BLAST results for sequences encoding polypeptides homologous to calpain p94; and
- (iii) the enclosed Appendix demonstrates that SEQ ID NO:10, rather than SEQ ID NO:32, has 24.9% identity to NCBI General Identifier Nos. 600420 and 1079058. (See, Table 5 and Example 3.) None of the other sequences in the application has 24.9% identity to NCBI General Identifier Nos. 600420 and 1079058.

Soybean Calpain p94 having clone designation ses9c.pk001.j23:fis

In the amended tables, SEQ ID NOs:33 and 34 were replaced, respectively, with SEQ ID NOs:11 and 12. This amendment is supported by the following:

- (i) the as-filed Sequence Listing indicates that SEQ ID NOs:11 and 12 are from soybean;
- (ii) originally filed Table 4 includes clone designation ses9c.pk001.j23:fis in the BLAST results for sequences encoding polypeptides homologous to calpain p94; and
- (iii) the enclosed Appendix demonstrates that SEQ ID NO:12, rather than SEQ ID NO:34, has 26.0% identity to NCBI General Identifier Nos. 600420 and 1079058. (See, Table 5 and Example 3.) None of the other sequences in the application has 26.0% identity to NCBI General Identifier Nos. 600420 and 1079058.

Rice Cysteine Protease 1 having clone designation rr1.pk084.j16:fis

In the amended tables, SEQ ID NOs:35 and 36 were replaced, respectively, with SEQ ID NOs:17 and 18. This amendment is supported by the following:

- (i) the as-filed Sequence Listing indicates that SEQ ID NOs:17 and 18 are from rice;
- (ii) originally filed Table 7 includes clone designation rr1.pk084.j16:fis in the BLAST results for sequences encoding polypeptides homologous to cysteine protease 1; and
- (iii) the enclosed Appendix demonstrates that SEQ ID NO:18, rather than SEQ ID NO:36, has 90.9% identity to NCBI General Identifier No. 1706260. (See, Table 8 and Example 4.) None of the other sequences in the application has 90.9% identity to NCBI General Identifier No. 1706260.

Wheat Cysteine Protease 1 having clone designation wek1c.pk009.j19:fis

In the amended tables, SEQ ID NO:37 and 38 were replaced, respectively, with SEQ ID NOs:19 and 20. This amendment is supported by the following:

- (i) the as-filed Sequence Listing indicates that SEQ ID NOs:19 and 20 are from wheat;

(ii) originally filed Table 7 includes clone designation wek1c.pk009.j19: fis in the BLAST results for sequences encoding polypeptides homologous to cysteine protease 1; and

(iii) the enclosed Appendix demonstrate that SEQ ID NO:20, rather than SEQ ID NO:38, has 86.3% identity to NCBI General Identifier No. 1706260. (See, Table 8 and Example 4.) None of the other sequences in the application has 86.3% identity to NCBI General Identifier No. 1706260.

Soybean Cysteine Protease 2 having clone designation srr3c.pk003.d10: fis

In the amended tables, SEQ ID NOs:39 and 40 were replaced, respectively, with SEQ ID NOs:23 and 24. This amendment is supported by the following:

(i) the as-filed Sequence Listing indicates that SEQ ID NOs:23 and 24 are from soybean;

(ii) originally filed Table 10 includes clone designation srr3c.pk003.d10: fis in the BLAST results for sequences encoding polypeptides homologous to cysteine protease 2; and

(iii) the enclosed Appendix demonstrates that SEQ ID NO:24, rather than SEQ ID NO:40, has 75.1% identity to NCBI General Identifier No. 2511691. (See, Table 11 and Example 5.) None of the other sequences in the application has 75.1% identity to NCBI General Identifier No. 2511691.

Corn CLP ATP Binding Subunit having clone designation p100.cgsmk69r: fis

In the amended tables, SEQ ID NOs:41 and 42 were replaced, respectively, with SEQ ID NOs:31 and 32. This amendment is supported by the following:

(i) the as-filed Sequence Listing indicates that SEQ ID NOs:31 and 32 are from corn;

(ii) originally filed Table 12 includes clone designation p100.cgsmk69r: fis in the BLAST results for sequences encoding polypeptides homologous to CLP protease ATP binding subunit; and

(iii) the enclosed Appendix demonstrates that SEQ ID NO:32, rather than SEQ ID NO:42, has 86.9% and 86.0% identity, respectively, to NCBI General Identifier Nos. 399213 and 399212. (See, Table 14 and Example 6.) None of the other sequences in the application has 86.9% and 86.0% identity, respectively, to NCBI General Identifier Nos. 399213 and 399212.

Rice CLP ATP Binding Subunit having clone designation rlr24.pk0088.f7: fis

In the amended tables, SEQ ID NOs:43 and 44 were replaced, respectively, with SEQ ID NOs:27 and 28. This amendment is supported by the following:

(i) the as-filed Sequence Listing indicates that SEQ ID NOs:27 and 28 are from rice;

(ii) originally filed Table 12 includes clone designation rlr24.pk0088.f7:fis in the BLAST results for sequences encoding polypeptides homologous to CLP protease ATP binding subunit; and

(iii) the enclosed Appendix demonstrates that SEQ ID NO:28, rather than SEQ ID NO:44, has 90.8% and 89.6% identity, respectively, to NCBI General Identifier Nos. 399213 and 399212. (See, Table 14 and Example 6.) None of the other sequences in the application has 90.8% and 89.6% identity, respectively, to NCBI General Identifier Nos. 399213 and 399212.

Wheat CLP ATP Binding Subunit having clone designation wlm96.pk032.n8:fis

In the amended tables, SEQ ID NOs:45 and 46 were replaced, respectively, with SEQ ID NOs:35 and 36. This amendment is supported by the following:

(i) the as-filed Sequence Listing indicates that SEQ ID NOs:35 and 36 are from wheat;  
(ii) originally filed Table 12 includes clone designation wlm96.pk032.n8:fis in the BLAST results for sequences encoding polypeptides homologous to CLP protease ATP binding subunit; and

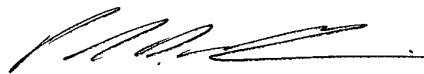
(iii) the enclosed Appendix demonstrates that SEQ ID NO:36, rather than SEQ ID NO:46, has 88.7% and 87.4% identity, respectively, to NCBI General Identifier Nos. 399213 and 399212. (See, Table 14 and Example 6.) None of the other sequences in the application has 88.7% and 87.4% identity, respectively, to NCBI General Identifier Nos. 399213 and 399212.

**Conclusion**

In view of the foregoing, it should be apparent that the amendments to the specification and claims are for the purpose of curing defects and it is submitted that these amendments are obvious to one skilled in the art. Entry of the amendments and favorable consideration of the claims are respectfully requested.

The Commissioner is authorized to charge Deposit Account No. 04-1928 (E. I. du Pont de Nemours and Company) for any requisite fees necessitated by this response.

Respectfully submitted,

  
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Dated: 2/15/02

**VERSION WITH MARKINGS TO SHOW CHANGES MADE**

In showing the changes, deleted material is shown in brackets and inserted material is shown double underlined.

**In the Specification:**

**Paragraph beginning at page 1, line 3:**

This application is a continuation of U.S. Application No. 09/501,423, filed February 9, 2000, which claims the benefit of U.S. Provisional Application No. 60/119,599, filed February 10, 1999, whose contents are hereby incorporated by reference.

**Paragraph beginning at page 2, line 13:**

The present invention relates to isolated polynucleotides comprising a nucleotide sequence encoding a polypeptide of at least 40 amino acids that has at least 85% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of a calpain p94 polypeptide of SEQ ID NOs:2, 4, 6, [30, 32, and 34]8, 10, and 12. The present invention also relates to an isolated polynucleotide comprising the complement of the nucleotide sequences described above.

**Paragraph beginning at page 2, line 19:**

The present invention relates to isolated polynucleotides comprising a nucleotide sequence encoding a polypeptide of at least 150 amino acids that has at least 95% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of a cysteine protease 1 polypeptide of SEQ ID NOs:[8, 10, 36, and 38]14, 16, 18, and 20. The present invention also relates to an isolated polynucleotide comprising the complement of the nucleotide sequences described above.

**Paragraph beginning at page 2, line 25:**

The present invention relates to isolated polynucleotides comprising a nucleotide sequence encoding a polypeptide of at least 200 amino acids that has at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of a cysteine protease 2 polypeptide of SEQ ID NOs:[12 and 40]22 and 24. The present invention also relates to an isolated polynucleotide comprising the complement of the nucleotide sequences described above.

**Paragraph beginning at page 2, line 31:**

The present invention relates to isolated polynucleotides comprising a nucleotide sequence encoding a polypeptide of at least 175 amino acids that has at least 95% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of a CLPA polypeptide of SEQ ID NOs:[14, 16, 18, 42, 44, and 46]26, 34, 30, 32, 28, and 36. The present invention also relates to an isolated polynucleotide comprising the complement of the nucleotide sequences described above.



**Paragraph beginning at page 2, line 37:**

The present invention relates to isolated polynucleotides comprising a nucleotide sequence encoding a CLPP polypeptide selected from the group consisting of SEQ ID NOs:[20, 22, 24, 26, 28,]38, 40, 42, 44, 46, 48, 50, 52, 54, and 56. The present invention also relates to an isolated polynucleotide comprising the complement of the nucleotide sequences described above.

**Paragraph beginning at page 3, line 25:**

The present invention relates to a calpain p94 polypeptide of at least 40 amino acids comprising at least 85% homology based on the Clustal method of alignment compared to a polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 6, [30, 32, and 34]8, 10, and 12.

**Paragraph beginning at page 3, line 28:**

The present invention relates to a cysteine protease 1 polypeptide of at least 150 amino acids comprising at least 95% homology based on the Clustal method of alignment compared to a polypeptide selected from the group consisting of SEQ ID NOs:[8, 10, 36, and 38]14, 16, 18, and 20.

**Paragraph beginning at page 3, line 32:**

The present invention relates to a cysteine protease 2 polypeptide of at least 200 amino acids comprising at least 80% homology based on the Clustal method of alignment compared to a polypeptide selected from the group consisting of SEQ ID NOs:[12 and 40]22 and 24.

**Paragraph beginning at page 3, line 35:**

The present invention relates to a CLPA polypeptide of at least 175 amino acids comprising at least 95% homology based on the Clustal method of alignment compared to a polypeptide selected from the group consisting of SEQ ID NOs:[14, 16, 18, 42, 44, and 46]26, 34, 30, 32, 28, and 36.

**Paragraph beginning at page 4, line 1:**

The present invention relates to a CLPP polypeptide selected from the group consisting of SEQ ID NOs:[20, 22, 24, 26, 28,]38, 40, 42, 44, 46, 48, 50, 52, 54, and 56.

**Table 1 bridging pages 5 and 6:**

TABLE 1  
PLANT PROTEINASES

Protein	Clone Designation	SEQ ID NO:	
		(Nucleotide)	(Amino Acid)
Corn Calpain p94 Subunit	cbn2.pk0039.c2	1	2
Rice Calpain p94 Subunit	rsl1n.pk013.h14	3	4
Soybean Calpain p94 Subunit	ses9c.pk001.j23	5	6
Rice Cysteine Protease 1	rr1.pk084.j16	[7] <u>13</u>	[8] <u>14</u>
Wheat Cysteine Protease 1	Contig of: wdk1c.pk009.j19	[9] <u>15</u>	[10] <u>16</u>

	wre1n.pk164.b11		
Soybean Cysteine Protease 2	Contig of: sgs2c.pk002.p14 srr3c.pk003.d10 scb1c.pk003.d8	[11] <u>21</u>	[12] <u>22</u>
Corn CLP ATP Binding Subunit	p0110.cgsmk69r	[13] <u>25</u>	[14] <u>26</u>
Rice CLP ATP Binding Subunit	Contig of: rlr6.pk0083.f9 rlr24.pk0088.f7 rlr6.pk0029.d7	[15] <u>33</u>	[16] <u>34</u>
Wheat CLP ATP Binding Subunit	wlm96.pk032.n8	[17] <u>29</u>	[18] <u>30</u>
Corn CLP Proteolytic Subunit	p0060.coran66r	[19] <u>37</u>	[20] <u>38</u>
Rice CLP Proteolytic Subunit	rsr9n.pk004.p5	[21] <u>39</u>	[22] <u>40</u>
Soybean CLP Proteolytic Subunit	scb1c.pk004.k24	[23] <u>41</u>	[24] <u>42</u>
Wheat CLP Proteolytic Subunit	wle1n.pk0042.f7	[25] <u>43</u>	[26] <u>44</u>
Wheat CLP Proteolytic Subunit	wlk8.pk0006.a4	[27] <u>45</u>	[28] <u>46</u>
Corn Calpain p94 Subunit	cbn2.pk0039.c2:fis	[29] <u>7</u>	[30] <u>8</u>
Rice Calpain p94 Subunit	rsl1n.pk013.h14:fis	[31] <u>9</u>	[32] <u>10</u>
Soybean Calpain p94 Subunit	ses9c.pk001.j23:fis	[33] <u>11</u>	[34] <u>12</u>
Rice Cysteine Protease 1	rr1.pk084.j16:fis	[35] <u>17</u>	[36] <u>18</u>
Wheat Cysteine Protease 1	wdk1c.pk009.j19:fis	[37] <u>19</u>	[38] <u>20</u>
Soybean Cysteine Protease 2	srr3c.pk003.d10:fis	[39] <u>23</u>	[40] <u>24</u>
Corn CLP ATP Binding Subunit	p0110.cgsmk69r:fis	[41] <u>31</u>	[42] <u>32</u>
Rice CLP ATP Binding Subunit	rlr24.pk0088.f7:fis	[43] <u>27</u>	[44] <u>28</u>
Wheat CLP ATP Binding Subunit	wlm96.pk032.n8:fis	[45] <u>35</u>	[46] <u>36</u>
Corn CLP Proteolytic Subunit	p0060.coran66r:fis	47	48
Rice CLP Proteolytic Subunit	rsr9n.pk004.p5:fis	49	50
Soybean CLP Proteolytic Subunit	scb1c.pk004.k24:fis	51	52
Wheat CLP Proteolytic Subunit	wle1n.pk0042.f7:fis	53	54
Wheat CLP Proteolytic Subunit	wlk8.pk0006.a4:fis	55	56

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**Paragraph beginning at page 22, line 16:**

The data in Table 5 represents a calculation of the percent identity of the amino acid sequences set forth in SEQ ID NOs:2, 4, 6, [30, 32, and 34]8, 10, and 12 and the *Drosophila melanogaster* sequences (NCBI General Identifier Nos. 600420 and 1079058).

**Table 5 beginning at page 22, line 20:**

TABLE 5		
Percent Identity of Amino Acid Sequences Deduced From the Nucleotide Sequences of cDNA Clones Encoding Polypeptides Homologous to Calpain p94		
SEQ ID NO.	Percent Identity to	
	600420	1079058
2	50.0	50.0
4	57.4	57.4
6	52.0	52.0
[30] 8	25.8	25.8
[32] 10	24.9	24.9
[34] 12	26.0	26.0

**Paragraph beginning at page 24, line 1:**

Amino acid sequence alignments using the Clustal method of alignment indicates that the rice sequence starts 88 amino acids down stream from the corn starting methionine, and that the wheat sequence starts 163 amino acids down stream from the corn starting methionine. The corn sequence has a signal sequence (amino acids 1-19) and a mature protein which corresponds to amino acids 137 through 371. Thus, the rice and wheat sequences included here contain the entire mature protein. The data in Table 8 represents a calculation of the percent identity of the amino acid sequences set forth in SEQ ID NOs:[8, 10, 36, and 38]14, 16, 18, and 20 and the *Zea mays* sequence (NCBI General Identifier No. 1706260).

**Table 8 beginning at page 24, line 10:**

TABLE 8	
Percent Identity of Amino Acid Sequences Deduced From the Nucleotide Sequences of cDNA Clones Encoding Polypeptides Homologous to Cysteine Protease 1	
SEQ ID NO.	Percent Identity to 1706260
[8] 14	88.0
[10] 16	87.1
[36] 18	90.9
[38] 20	86.3

**Paragraph beginning at page 25, line 16:**

The data in Table 11 represents a calculation of the percent identity of the amino acid sequences set forth in SEQ ID NOs:[12 and 40]22 and 24 and the *Phaseolus vulgaris* sequence (NCBI General Identifier No. 2511691).

**Table 11 beginning at page 25, line 20:**

TABLE 11

Percent Identity of Amino Acid Sequences Deduced From the Nucleotide  
Sequences of cDNA Clones Encoding Polypeptides  
Homologous to Cysteine Protease 2

SEQ ID NO.	Percent Identity to 2511691
[12] <u>22</u>	67.9
[40] <u>24</u>	75.1

**Paragraph beginning at page 27, line 5:**

The data in Table 14 represents a calculation of the percent identity of the amino acid sequences set forth in SEQ ID NOs:[14, 16, 18, 42, 44, and 46]26, 34, 30, 32, 28, and 36 and the *Lycopersicon esculentum* sequences (NCBI General Identifier Nos. 399213 and 399212).

**Table 14 beginning at page 27, line 9:**

TABLE 14

Percent Identity of Amino Acid Sequences Deduced From the Nucleotide  
Sequences of cDNA Clones Encoding Polypeptides  
Homologous to CLP Protease ATP-Binding Subunit

SEQ ID NO.	Percent Identity to	
	399213	399212
[14] <u>26</u>	92.2	92.2
[16] <u>34</u>	80.9	79.9
[18] <u>30</u>	86.5	87.1
[42] <u>32</u>	86.9	86.0
[44] <u>28</u>	90.8	89.6
[46] <u>36</u>	88.7	87.4

**Paragraph beginning at page 28, line 26:**

The data in Table 17 represents a calculation of the percent identity of the amino acid sequences set forth in SEQ ID NOs:[20, 22, 24, 26, 28,]38, 40, 42, 44, 46, 48, 50, 52, 54, and 56 and the *Arabidopsis thaliana* and *Azospirillum brasilense* sequences (NCBI General Identifier Nos. 5360593, 4887543, and 6685315).

**Table 17 beginning at page 29, line 4:**

**TABLE 17**

Percent Identity of Amino Acid Sequences Deduced From the Nucleotide  
Sequences of cDNA Clones Encoding Polypeptides  
Homologous to CLP Protease Proteolytic Subunit

SEQ ID NO.	Percent Identity to		
	5360593	4887543	6685315
[20] <u>38</u>	78.8	52.2	53.1
[22] <u>40</u>	44.0	55.0	73.4
[24] <u>42</u>	48.7	97.3	58.7
[26] <u>44</u>	55.8	91.6	63.2
[28] <u>46</u>	57.1	64.3	81.0
48	78.8	39.7	38.6
50	34.0	43.8	57.6
52	45.5	92.5	51.5
54	39.0	47.1	60.5
56	48.9	87.9	54.6

**In the Claims:**

**Please replace the following claims:**

1. “amended” An isolated polynucleotide comprising a first nucleotide sequence encoding a polypeptide of at least 40 amino acids that has at least 85% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 6, [30, 32, and 34]8, 10, and 12,

or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

2. “amended” An isolated polynucleotide comprising a first nucleotide sequence encoding a polypeptide of at least 150 amino acids that has at least 95% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:[8, 10, 36, and 38]14, 16, 18, and 20,

or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

3. “amended” An isolated polynucleotide comprising a first nucleotide sequence encoding a polypeptide of at least 200 amino acids that has at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:[12 and 40]22 and 24,

or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

4. “amended” An isolated polynucleotide comprising a first nucleotide sequence encoding a polypeptide of at least 175 amino acids that has at least 95% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:[14, 16, 18, 42, 44, and 46]26, 34, 30, 32, 28, and 36,

or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

5. “amended” An isolated polynucleotide comprising a first nucleotide sequence encoding a polypeptide selected from the group consisting of SEQ ID NOs:[20, 22, 24, 26, 28,]38, 40, 42, 44, 46, 48, 50, 52, 54, and 56,

or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

14. “amended” A polypeptide of at least 40 amino acids that has at least 85% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 6, [30, 32, and 34]8, 10, and 12.

15. “amended” A polypeptide of at least 150 amino acids that has at least 95% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:[8, 10, 36, and 38]14, 16, 18, 20.

16. “amended” A polypeptide of at least 200 amino acids that has at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:[12 and 40]22 and 24.

17. “amended” A polypeptide of at least 175 amino acids that has at least 95% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:[14, 16, 18, 42, 44, and 46]26, 34, 30, 32, 28, and 36.

18. “amended” A polypeptide selected from the group consisting of SEQ ID NOs:[20, 22, 24, 26, 28,]38, 40, 42, 44, 46, 48, 50, 52, 54, and 56.

#### IN THE ABSTRACT:

**Please replace the paragraph beginning at page 39, line 4, with the following replacement paragraph:**

[This invention relates to an isolated nucleic acid fragment] Isolated polynucleotides from corn (*Zea mays*), rice (*Oryza sativa*), soybean (*Glycine max*), and wheat (*Triticum aestivum*) encoding [a] proteinases. [The invention also relates to] Also provided is the construction of a chimeric gene encoding all or a portion of the proteinase, in sense or antisense orientation, wherein expression of the chimeric gene results in production of altered levels of the proteinase in a transformed host cell.

APPENDIX  
Percent Identity Obtained Using Clustal Alignment Method

SEQ ID NO:	NCBI General Identifier No.									
	600420	1079058	1706260	2511691	399213	399212	5360593	4887543	6685315	
2	50.0	50.0	20.7	17.2	20.7	19.0	17.2	15.5	17.2	
4	57.4	57.4	23.4	19.1	21.3	21.3	17.0	14.9	19.1	
6	52.0	52.0	22.0	18.0	20.0	20.0	18.0	0.0	18.0	
8	25.8	25.8	10.1	9.2	12.2	11.9	11.4	11.7	11.4	
10	24.9	24.9	10.4	9.2	11.9	12.2	11.0	12.1	12.9	
12	26.0	26.0	9.9	10.5	12.0	11.7	11.0	12.4	14.3	
14	14.4	13.8	88.0	65.3	15.0	15.0	13.2	10.8	11.4	
16	15.3	14.4	87.1	75.1	13.4	13.4	11.5	10.5	10.5	
18	12.6	13.3	90.9	69.6	12.2	12.9	10.5	10.1	11.9	
20	12.7	14.2	86.3	74.5	13.2	13.7	12.7	10.8	10.5	
22	12.8	13.2	58.1	67.9	14.1	13.7	13.7	11.5	10.5	
24	10.4	10.9	64.8	75.1	12.6	11.5	10.7	13.1	11.9	
26	15.6	15.6	12.5	12.5	92.2	92.2	14.8	14.1	12.5	
28	10.4	10.7	12.7	12.1	90.8	89.6	11.7	11.4	15.7	
30	12.9	12.9	14.0	12.9	86.5	87.1	12.4	11.2	11.2	
32	11.6	11.5	11.9	10.4	86.9	86.0	11.0	11.1	14.8	
34	12.4	12.4	13.8	13.1	80.9	79.9	11.7	10.4	13.3	
36	13.4	13.4	12.6	11.3	88.7	87.4	11.7	10.0	12.9	
38	16.8	16.8	13.3	15.0	16.8	16.8	78.8	52.2	53.1	
40	14.7	14.7	11.9	14.7	15.6	18.3	44.0	55.0	73.4	
42	14.0	14.0	13.3	14.0	12.7	12.0	48.7	97.3	58.7	
44	15.8	15.8	14.7	14.7	14.7	13.7	55.8	91.6	63.2	
46	15.5	15.5	15.5	14.3	17.9	20.2	57.1	64.3	81.0	
48	14.8	14.8	11.6	12.7	15.9	14.8	78.8	39.7	38.6	
50	13.9	13.9	12.5	12.5	16.0	15.3	34.0	43.8	57.6	
52	13.5	13.5	10.5	13.5	12.0	11.5	45.5	92.5	51.5	
54	14.5	14.5	12.8	14.0	11.6	11.6	49.4	89.0	55.2	
56	13.4	13.4	11.6	11.0	13.4	14.0	39.0	47.1	60.5	